

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of Desnoyers, et al. Serial No.: Filed herewith Filed: August 16, 2001 For: <i>SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME</i>	Group Art Unit: Unknown Examiner: Unknown Express Mail No. EL 895 375 396 US Filed on August 16, 2001
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CERTIFICATE RE: SEQUENCE LISTING

RESPONSE UNDER 37 CFR § 1.821(f) and (g)

Box: Patent Application
Assistant Commissioner of Patents
Washington, D.C. 20231

Sir:

I hereby state that the Sequence Listing submitted herewith is submitted in paper copy and a computer-readable diskette, and that the information recorded in computer readable form is identical to the written sequence listing. I further state that this submission includes no new matter.

Respectfully submitted,

GENENTECH, INC.

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Date: August 16, 2001



09157

PATENT TRADEMARK OFFICE

Sequence Listing

<110> Desnoyers, Luc
 Eaton, Dan L.
 Goddard, Audrey
 Godowski, Paul J.
 Gurney, Austin L.
 Pan, James
 Stewart, Timothy A.
 Watanabe, Colin K.
 Wood, William I.
 Zhang, Zemin

<120> SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ACIDS ENCODING THE SAME

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<210> 18

<211> 273

<212> PRT

<213> Homo Sapien

<400> 18

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Cys	Phe	Ala	Asp	Phe	Lys	His	Pro	Cys	Tyr	Lys	Met	Ala	Tyr	Phe	35	40	45	
His	Glu	Leu	Ser	Ser	Arg	Val	Ser	Phe	Gln	Glu	Ala	Arg	Leu	Ala	50	55	60	
Cys	Glu	Ser	Glu	Gly	Gly	Val	Leu	Leu	Ser	Leu	Glu	Asn	Glu	Ala	65	70	75	
Glu	Gln	Lys	Leu	Ile	Glu	Ser	Met	Leu	Gln	Asn	Leu	Thr	Lys	Pro	80	85	90	
Gly	Thr	Gly	Ile	Ser	Asp	Gly	Asp	Phe	Trp	Ile	Gly	Leu	Trp	Arg	95	100	105	
Asn	Gly	Asp	Gly	Gln	Thr	Ser	Gly	Ala	Cys	Pro	Asp	Leu	Tyr	Gln	110	115	120	
Trp	Ser	Asp	Gly	Ser	Asn	Ser	Gln	Tyr	Arg	Asn	Trp	Tyr	Thr	Asp	125	130	135	
Glu	Pro	Ser	Cys	Gly	Ser	Glu	Lys	Cys	Val	Val	Met	Tyr	His	Gln	140	145	150	
Pro	Thr	Ala	Asn	Pro	Gly	Leu	Gly	Gly	Pro	Tyr	Leu	Tyr	Gln	Trp	155	160	165	
Asn	Asp	Asp	Arg	Cys	Asn	Met	Lys	His	Asn	Tyr	Ile	Cys	Lys	Tyr				

170	175	180
Glu Pro Glu Ile Asn Pro Thr Ala Pro	Val Glu Lys Pro Tyr Leu	
185	190	195
Thr Asn Gln Pro Gly Asp Thr His Gln	Asn Val Val Val Thr Glu	
200	205	210
Ala Gly Ile Ile Pro Asn Leu Ile Tyr	Val Val Ile Pro Thr Ile	
215	220	225
Pro Leu Leu Leu Leu Ile Leu Val Ala	Phe Gly Thr Cys Cys Phe	
230	235	240
Gln Met Leu His Lys Ser Lys Gly Arg	Thr Lys Thr Ser Pro Asn	
245	250	255
Gln Ser Thr Leu Trp Ile Ser Lys Ser	Thr Arg Lys Glu Ser Gly	
260	265	270
Met Glu Val		

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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 19
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<210> 20
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 <212> DNA
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<220>
 <223> Synthetic oligonucleotide probe

<400> 20
 accacattct gatgggtgtc tctctgg 26

<210> 21
 <211> 49
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 21
 ggggtccctac ctttaccagt ggaatgatga caggtgtaac atgaagcac 49

<210> 22
 <211> 3824

<212> DNA

<213> Homo Sapien

<400> 22

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gcgtgaaggg cacagaccgc cttgtgaatg tctttctggg cattccattt 200
gcccagccgc cactgggccc tgaccggttc tcagccccac acccagcaca 250
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 aataaatctt gctactgccc aaaa 3824

<210> 23

<211> 571

<212> PRT

<213> Homo Sapien

<400> 23

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				20					25				30	
Val	Ala	Gln	Pro	Glu	Val	Asp	Thr	Thr	Leu	Gly	Arg	Val	Arg	Gly
				35					40				45	
Arg	Gln	Val	Gly	Val	Lys	Gly	Thr	Asp	Arg	Leu	Val	Asn	Val	Phe

1000
 900
 800
 700
 600
 500
 400
 300
 200
 100
 0

50										55					60				
Leu	Gly	Ile	Pro	Phe	Ala	Gln	Pro	Pro	Leu	Gly	Pro	Asp	Arg	Phe					
65										70					75				
Ser	Ala	Pro	His	Pro	Ala	Gln	Pro	Trp	Glu	Gly	Val	Arg	Asp	Ala					
80										85					90				
Ser	Thr	Ala	Pro	Pro	Met	Cys	Leu	Gln	Asp	Val	Glu	Ser	Met	Asn					
95										100					105				
Ser	Ser	Arg	Phe	Val	Leu	Asn	Gly	Lys	Gln	Gln	Ile	Phe	Ser	Val					
110										115					120				
Ser	Glu	Asp	Cys	Leu	Val	Leu	Asn	Val	Tyr	Ser	Pro	Ala	Glu	Val					
125										130					135				
Pro	Ala	Gly	Ser	Gly	Arg	Pro	Val	Met	Val	Trp	Val	His	Gly	Gly					
140										145					150				
Ala	Leu	Ile	Thr	Gly	Ala	Ala	Thr	Ser	Tyr	Asp	Gly	Ser	Ala	Leu					
155										160					165				
Ala	Ala	Tyr	Gly	Asp	Val	Val	Val	Val	Thr	Val	Gln	Tyr	Arg	Leu					
170										175					180				
Gly	Val	Leu	Gly	Phe	Phe	Ser	Thr	Gly	Asp	Glu	His	Ala	Pro	Gly					
185										190					195				
Asn	Gln	Gly	Phe	Leu	Asp	Val	Val	Ala	Ala	Leu	Arg	Trp	Val	Gln					
200										205					210				
Glu	Asn	Ile	Ala	Pro	Phe	Gly	Gly	Asp	Leu	Asn	Cys	Val	Thr	Val					
215										220					225				
Phe	Gly	Gly	Ser	Ala	Gly	Gly	Ser	Ile	Ile	Ser	Gly	Leu	Val	Leu					
230										235					240				
Ser	Pro	Val	Ala	Ala	Gly	Leu	Phe	His	Arg	Ala	Ile	Thr	Gln	Ser					
245										250					255				
Gly	Val	Ile	Thr	Thr	Pro	Gly	Ile	Ile	Asp	Ser	His	Pro	Trp	Pro					
260										265					270				
Leu	Ala	Gln	Lys	Ile	Ala	Asn	Thr	Leu	Ala	Cys	Ser	Ser	Ser	Ser					
275										280					285				
Pro	Ala	Glu	Met	Val	Gln	Cys	Leu	Gln	Gln	Lys	Glu	Gly	Glu	Glu					
290										295					300				
Leu	Val	Leu	Ser	Lys	Lys	Leu	Lys	Asn	Thr	Ile	Tyr	Pro	Leu	Thr					
305										310					315				
Val	Asp	Gly	Thr	Val	Phe	Pro	Lys	Ser	Pro	Lys	Glu	Leu	Leu	Lys					
320										325					330				
Glu	Lys	Pro	Phe	His	Ser	Val	Pro	Phe	Leu	Met	Gly	Val	Asn	Asn					
335										340					345				

His	Glu	Phe	Ser	Trp	Leu	Ile	Pro	Arg	Gly	Trp	Gly	Leu	Leu	Asp	350	355	360
Thr	Met	Glu	Gln	Met	Ser	Arg	Glu	Asp	Met	Leu	Ala	Ile	Ser	Thr	365	370	375
Pro	Val	Leu	Thr	Ser	Leu	Asp	Val	Pro	Pro	Glu	Met	Met	Pro	Thr	380	385	390
Val	Ile	Asp	Glu	Tyr	Leu	Gly	Ser	Asn	Ser	Asp	Ala	Gln	Ala	Lys	395	400	405
Cys	Gln	Ala	Phe	Gln	Glu	Phe	Met	Gly	Asp	Val	Phe	Ile	Asn	Val	410	415	420
Pro	Thr	Val	Ser	Phe	Ser	Arg	Tyr	Leu	Arg	Asp	Ser	Gly	Ser	Pro	425	430	435
Val	Phe	Phe	Tyr	Glu	Phe	Gln	His	Arg	Pro	Ser	Ser	Phe	Ala	Lys	440	445	450
Ile	Lys	Pro	Ala	Trp	Val	Lys	Ala	Asp	His	Gly	Ala	Glu	Gly	Ala	455	460	465
Phe	Val	Phe	Gly	Gly	Pro	Phe	Leu	Met	Asp	Glu	Ser	Ser	Arg	Leu	470	475	480
Ala	Phe	Pro	Glu	Ala	Thr	Glu	Glu	Glu	Lys	Gln	Leu	Ser	Leu	Thr	485	490	495
Met	Met	Ala	Gln	Trp	Thr	His	Phe	Ala	Arg	Thr	Gly	Asp	Pro	Asn	500	505	510
Ser	Lys	Ala	Leu	Pro	Pro	Trp	Pro	Gln	Phe	Asn	Gln	Ala	Glu	Gln	515	520	525
Tyr	Leu	Glu	Ile	Asn	Pro	Val	Pro	Arg	Ala	Gly	Gln	Lys	Phe	Arg	530	535	540
Glu	Ala	Trp	Met	Gln	Phe	Trp	Ser	Glu	Thr	Leu	Pro	Ser	Lys	Ile	545	550	555
Gln	Gln	Trp	His	Gln	Lys	Gln	Lys	Asn	Arg	Lys	Ala	Gln	Glu	Asp	560	565	570

Leu

<210> 24

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 24

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<210> 25
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 25
gggtggactg tgctctaata gacgc 25

<210> 26
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 26
cgtggcactg gggtgatc 18

<210> 27
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 27
gatgcagttc tggtcagaga cgctccccag caagatacaa cagtg 45

<210> 28
<211> 1342
<212> DNA
<213> Homo Sapien

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cttctacaac taaaattcct caaacctaaa atcaacagct tttatgcctt 150
tgaagtgaag gatgcaaaaag gaagaactgt ttctctggaa aagtataaag 200
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agaaattact tagggctgaa ggaactgcac aaagagtttg gaccatccca 300
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<210> 29
 <211> 209
 <212> PRT
 <213> Homo Sapien

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 20 25 30
 Thr Leu Phe Leu Leu Gln Leu Lys Phe Leu Lys Pro Lys Ile Asn
 35 40 45
 Ser Phe Tyr Ala Phe Glu Val Lys Asp Ala Lys Gly Arg Thr Val
 50 55 60
 Ser Leu Glu Lys Tyr Lys Gly Lys Val Ser Leu Val Val Asn Val
 65 70 75
 Ala Ser Asp Cys Gln Leu Thr Asp Arg Asn Tyr Leu Gly Leu Lys
 80 85 90

Glu	Leu	His	Lys	Glu	Phe	Gly	Pro	Ser	His	Phe	Ser	Val	Leu	Ala
				95					100					105
Phe	Pro	Cys	Asn	Gln	Phe	Gly	Glu	Ser	Glu	Pro	Arg	Pro	Ser	Lys
				110					115					120
Glu	Val	Glu	Ser	Phe	Ala	Arg	Lys	Asn	Tyr	Gly	Val	Thr	Phe	Pro
				125					130					135
Ile	Phe	His	Lys	Ile	Lys	Ile	Leu	Gly	Ser	Glu	Gly	Glu	Pro	Ala
				140					145					150
Phe	Arg	Phe	Leu	Val	Asp	Ser	Ser	Lys	Lys	Glu	Pro	Arg	Trp	Asn
				155					160					165
Phe	Trp	Lys	Tyr	Leu	Val	Asn	Pro	Glu	Gly	Gln	Val	Val	Lys	Phe
				170					175					180
Trp	Arg	Pro	Glu	Glu	Pro	Ile	Glu	Val	Ile	Arg	Pro	Asp	Ile	Ala
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

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<210> 31
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<220>
 <223> Synthetic oligonucleotide probe

<400> 31
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<210> 32
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 <212> DNA
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<220>
 <223> Synthetic oligonucleotide probe

<400> 32
 taaccagagc tgctatgtca ggcc 24

<210> 33

<211> 50
<212> DNA
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<210> 34
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<212> DNA
<213> Homo Sapien

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<210> 35

<211> 888

<212> PRT

<213> Homo Sapien

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				20					25					30	
Pro	Pro	Pro	Leu	Ser	Val	Ala	Pro	Arg	Asp	Tyr	Leu	Asn	His	Tyr	
				35					40					45	
Pro	Val	Phe	Val	Gly	Ser	Gly	Pro	Gly	Arg	Leu	Thr	Pro	Ala	Glu	
				50					55					60	
Gly	Ala	Asp	Asp	Leu	Asn	Ile	Gln	Arg	Val	Leu	Arg	Val	Asn	Arg	
				65					70					75	
Thr	Leu	Phe	Ile	Gly	Asp	Arg	Asp	Asn	Leu	Tyr	Arg	Val	Glu	Leu	
				80					85					90	
Glu	Pro	Pro	Thr	Ser	Thr	Glu	Leu	Arg	Tyr	Gln	Arg	Lys	Leu	Thr	
				95					100					105	
Trp	Arg	Ser	Asn	Pro	Ser	Asp	Ile	Asn	Val	Cys	Arg	Met	Lys	Gly	
				110					115					120	
Lys	Gln	Glu	Gly	Glu	Cys	Arg	Asn	Phe	Val	Lys	Val	Leu	Leu	Leu	
				125					130					135	
Arg	Asp	Glu	Ser	Thr	Leu	Phe	Val	Cys	Gly	Ser	Asn	Ala	Phe	Asn	
				140					145					150	
Pro	Val	Cys	Ala	Asn	Tyr	Ser	Ile	Asp	Thr	Leu	Gln	Pro	Val	Gly	
				155					160					165	
Asp	Asn	Ile	Ser	Gly	Met	Ala	Arg	Cys	Pro	Tyr	Asp	Pro	Lys	His	
				170					175					180	
Ala	Asn	Val	Ala	Leu	Phe	Ser	Asp	Gly	Met	Leu	Phe	Thr	Ala	Thr	
				185					190					195	
Val	Thr	Asp	Phe	Leu	Ala	Ile	Asp	Ala	Val	Ile	Tyr	Arg	Ser	Leu	
				200					205					210	
Gly	Asp	Arg	Pro	Thr	Leu	Arg	Thr	Val	Lys	His	Asp	Ser	Lys	Trp	
				215					220					225	
Phe	Lys	Glu	Pro	Tyr	Phe	Val	His	Ala	Val	Glu	Trp	Gly	Ser	His	
				230					235					240	
Val	Tyr	Phe	Phe	Phe	Arg	Glu	Ile	Ala	Met	Glu	Phe	Asn	Tyr	Leu	
				245					250					255	
Glu	Lys	Val	Val	Val	Ser	Arg	Val	Ala	Arg	Val	Cys	Lys	Asn	Asp	
				260					265					270	
Val	Gly	Gly	Ser	Pro	Arg	Val	Leu	Glu	Lys	Gln	Trp	Thr	Ser	Phe	
				275					280					285	
Leu	Lys	Ala	Arg	Leu	Asn	Cys	Ser	Val	Pro	Gly	Asp	Ser	His	Phe	
				290					295					300	
Tyr	Phe	Asn	Val	Leu	Gln	Ala	Val	Thr	Gly	Val	Val	Ser	Leu	Gly	

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				320					325					330
Ile	Pro	Gly	Ser	Ala	Val	Cys	Ala	Phe	Asp	Leu	Thr	Gln	Val	Ala
				335					340					345
Ala	Val	Phe	Glu	Gly	Arg	Phe	Arg	Glu	Gln	Lys	Ser	Pro	Glu	Ser
				350					355					360
Ile	Trp	Thr	Pro	Val	Pro	Glu	Asp	Gln	Val	Pro	Arg	Pro	Arg	Pro
				365					370					375
Gly	Cys	Cys	Ala	Ala	Pro	Gly	Met	Gln	Tyr	Asn	Ala	Ser	Ser	Ala
				380					385					390
Leu	Pro	Asp	Asp	Ile	Leu	Asn	Phe	Val	Lys	Thr	His	Pro	Leu	Met
				395					400					405
Asp	Glu	Ala	Val	Pro	Ser	Leu	Gly	His	Ala	Pro	Trp	Ile	Leu	Arg
				410					415					420
Thr	Leu	Met	Arg	His	Gln	Leu	Thr	Arg	Val	Ala	Val	Asp	Val	Gly
				425					430					435
Ala	Gly	Pro	Trp	Gly	Asn	Gln	Thr	Val	Val	Phe	Leu	Gly	Ser	Glu
				440					445					450
Ala	Gly	Thr	Val	Leu	Lys	Phe	Leu	Val	Arg	Pro	Asn	Ala	Ser	Thr
				455					460					465
Ser	Gly	Thr	Ser	Gly	Leu	Ser	Val	Phe	Leu	Glu	Glu	Phe	Glu	Thr
				470					475					480
Tyr	Arg	Pro	Asp	Arg	Cys	Gly	Arg	Pro	Gly	Gly	Gly	Glu	Thr	Gly
				485					490					495
Gln	Arg	Leu	Leu	Ser	Leu	Glu	Leu	Asp	Ala	Ala	Ser	Gly	Gly	Leu
				500					505					510
Leu	Ala	Ala	Phe	Pro	Arg	Cys	Val	Val	Arg	Val	Pro	Val	Ala	Arg
				515					520					525
Cys	Gln	Gln	Tyr	Ser	Gly	Cys	Met	Lys	Asn	Cys	Ile	Gly	Ser	Gln
				530					535					540
Asp	Pro	Tyr	Cys	Gly	Trp	Ala	Pro	Asp	Gly	Ser	Cys	Ile	Phe	Leu
				545					550					555
Ser	Pro	Gly	Thr	Arg	Ala	Ala	Phe	Glu	Gln	Asp	Val	Ser	Gly	Ala
				560					565					570
Ser	Thr	Ser	Gly	Leu	Gly	Asp	Cys	Thr	Gly	Leu	Leu	Arg	Ala	Ser
				575					580					585
Leu	Ser	Glu	Asp	Arg	Ala	Gly	Leu	Val	Ser	Val	Asn	Leu	Leu	Val
				590					595					600

Thr Ser Ser Val	Ala Ala Phe Val Val	Gly Ala Val Val Ser Gly	605	610	615
Phe Ser Val Gly	Trp Phe Val Gly Leu	Arg Glu Arg Arg Glu Leu	620	625	630
Ala Arg Arg Lys	Asp Lys Glu Ala Ile	Leu Ala His Gly Ala Gly	635	640	645
Glu Ala Val Leu	Ser Val Ser Arg Leu	Gly Glu Arg Arg Ala Gln	650	655	660
Gly Pro Gly Gly	Arg Gly Gly Gly Gly	Gly Gly Gly Ala Gly Val	665	670	675
Pro Pro Glu Ala	Leu Leu Ala Pro Leu	Met Gln Asn Gly Trp Ala	680	685	690
Lys Ala Thr Leu	Leu Gln Gly Gly Pro	His Asp Leu Asp Ser Gly	695	700	705
Leu Leu Pro Thr	Pro Glu Gln Thr Pro	Leu Pro Gln Lys Arg Leu	710	715	720
Pro Thr Pro His	Pro His Pro His Ala	Leu Gly Pro Arg Ala Trp	725	730	735
Asp His Gly His	Pro Leu Leu Pro Ala	Ser Ala Ser Ser Ser Leu	740	745	750
Leu Leu Leu Ala	Pro Ala Arg Ala Pro	Glu Gln Pro Pro Ala Pro	755	760	765
Gly Glu Pro Thr	Pro Asp Gly Arg Leu	Tyr Ala Ala Arg Pro Gly	770	775	780
Arg Ala Ser His	Gly Asp Phe Pro Leu	Thr Pro His Ala Ser Pro	785	790	795
Asp Arg Arg Arg	Val Val Ser Ala Pro	Thr Gly Pro Leu Asp Pro	800	805	810
Ala Ser Ala Ala	Asp Gly Leu Pro Arg	Pro Trp Ser Pro Pro Pro	815	820	825
Thr Gly Ser Leu	Arg Arg Pro Leu Gly	Pro His Ala Pro Pro Ala	830	835	840
Ala Thr Leu Arg	Arg Thr His Thr Phe	Asn Ser Gly Glu Ala Arg	845	850	855
Pro Gly Asp Arg	His Arg Gly Cys His	Ala Arg Pro Gly Thr Asp	860	865	870
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 35 40 45
 Pro Ala Arg Tyr Phe Tyr Ile Gln Ala Val Asp Thr Ser Gly Asn
 50 55 60
 Lys Phe Thr Ser Ser Pro Gly Glu Lys Val Phe Gln Val Lys Val
 65 70 75
 Ser Ala Pro Glu Glu Gln Phe Thr Arg Val Gly Val Gln Val Leu
 80 85 90
 Asp Arg Lys Asp Gly Ser Phe Ile Val Arg Tyr Arg Met Tyr Ala
 95 100 105
 Ser Tyr Lys Asn Leu Lys Val Glu Ile Lys Phe Gln Gly Gln His
 110 115 120
 Val Ala Lys Ser Pro Tyr Ile Leu Lys Gly Pro Val Tyr His Glu
 125 130 135
 Asn Cys Asp Cys Pro Leu Gln Asp Ser Ala Ala Trp Leu Arg Glu
 140 145 150
 Met Asn Cys Pro Glu Thr Ile Ala Gln Ile Gln Arg Asp Leu Ala
 155 160 165
 His Phe Pro Ala Val Asp Pro Glu Lys Ile Ala Val Glu Ile Pro
 170 175 180
 Lys Arg Phe Gly Gln Arg Gln Ser Leu Cys His Tyr Thr Leu Lys
 185 190 195
 Asp Asn Lys Val Tyr Ile Lys Thr His Gly Glu His Val Gly Phe
 200 205 210
 Arg Ile Phe Met Asp Ala Ile Leu Leu Ser Leu Thr Arg Lys Val
 215 220 225
 Lys Met Pro Asp Val Glu Leu Phe Val Asn Leu Gly Asp Trp Pro

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230	235	240
Leu Glu Lys Lys Lys Ser Asn Ser Asn	Ile His Pro Ile Phe Ser	
245	250	255
Trp Cys Gly Ser Thr Asp Ser Lys Asp	Ile Val Met Pro Thr Tyr	
260	265	270
Asp Leu Thr Asp Ser Val Leu Glu Thr	Met Gly Arg Val Ser Leu	
275	280	285
Asp Met Met Ser Val Gln Ala Asn Thr	Gly Pro Pro Trp Glu Ser	
290	295	300
Lys Asn Ser Thr Ala Val Trp Arg Gly	Arg Asp Ser Arg Lys Glu	
305	310	315
Arg Leu Glu Leu Val Lys Leu Ser Arg	Lys His Pro Glu Leu Ile	
320	325	330
Asp Ala Ala Phe Thr Asn Phe Phe Phe	Phe Lys His Asp Glu Asn	
335	340	345
Leu Tyr Gly Pro Ile Val Lys His Ile	Ser Phe Phe Asp Phe Phe	
350	355	360
Lys His Lys Tyr Gln Ile Asn Ile Asp	Gly Thr Val Ala Ala Tyr	
365	370	375
Arg Leu Pro Tyr Leu Leu Val Gly Asp	Ser Val Val Leu Lys Gln	
380	385	390
Asp Ser Ile Tyr Tyr Glu His Phe Tyr	Asn Glu Leu Gln Pro Trp	
395	400	405
Lys His Tyr Ile Pro Val Lys Ser Asn	Leu Ser Asp Leu Leu Glu	
410	415	420
Lys Leu Lys Trp Ala Lys Asp His Asp	Glu Glu Ala Lys Lys Ile	
425	430	435
Ala Lys Ala Gly Gln Glu Phe Ala Arg	Asn Asn Leu Met Gly Asp	
440	445	450
Asp Ile Phe Cys Tyr Tyr Phe Lys Leu	Phe Gln Glu Tyr Ala Asn	
455	460	465
Leu Gln Val Ser Glu Pro Gln Ile Arg	Glu Gly Met Lys Arg Val	
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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 41
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<210> 42
<211> 24
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 42
cgataagctg ctacagtgcc atcg 24

<210> 43
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 43
gtgactgtcc tctgcaagat agtgcagcct ggctacggga 40

<210> 44
<211> 2395
<212> DNA
<213> Homo Sapien

<400> 44
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tcgctacctg ttgcgtagcg atcgaggtgc tagggatcgc ggtcttcctt 150
cggggattct tcccggctcc cgttcgttcc tctgccagag cggaacacgg 200
agcggagccc ccagcgcggc aaccctcggc tggagccagt tctaactgga 250
ccacgctgcc accacctctc ttcagtaaag ttgttattgt tctgatagat 300
gccttgagag atgattttgt gtttggggtca aaggggtgtga aatttatgcc 350
ctacacaact taccttgtgg aaaaaggagc atctcacagt tttgtggctg 400
aagcaaagcc acctacagtt actatgcctc gaatcaaggc attgatgacg 450
gggagccttc ctggctttgt cgacgtcatc aggaacctca attctcctgc 500
actgctggaa gacagtgtga taagacaagc aaaagcagct ggaaaaagaa 550

tcttagtcct tggcctcgga caccttcatt cgtagctgg ggagtgggtgg 2050
 tgaggcagtg aagaagaggc ggatgggtcac actcagatcc acagagccca 2100
 ggatcaaggg acccactgca gtggcagcag gactgttggg cccccacccc 2150
 aacctgcac agccctcatc cctctttggc ttgagccgtc agaggccctg 2200
 tgctgagtgt ctgaccgaga cactcacagc tttgtcatca gggcacaggc 2250
 ttctcggag ccaggatgat ctgtgccacg cttgcacctc gggcccatct 2300
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 tatgtagtta ccaaaagaat aaacggcaat aattgagaaa aaaaa 2395

<210> 45

<211> 310

<212> PRT

<213> Homo Sapien

<400> 45

Met	Arg	Leu	Gly	Ser	Gly	Thr	Phe	Ala	Thr	Cys	Cys	Val	Ala	Ile
1				5					10					15
Glu	Val	Leu	Gly	Ile	Ala	Val	Phe	Leu	Arg	Gly	Phe	Phe	Pro	Ala
			20						25					30
Pro	Val	Arg	Ser	Ser	Ala	Arg	Ala	Glu	His	Gly	Ala	Glu	Pro	Pro
			35						40					45
Ala	Pro	Glu	Pro	Ser	Ala	Gly	Ala	Ser	Ser	Asn	Trp	Thr	Thr	Leu
			50						55					60
Pro	Pro	Pro	Leu	Phe	Ser	Lys	Val	Val	Ile	Val	Leu	Ile	Asp	Ala
			65						70					75
Leu	Arg	Asp	Asp	Phe	Val	Phe	Gly	Ser	Lys	Gly	Val	Lys	Phe	Met
			80						85					90
Pro	Tyr	Thr	Thr	Tyr	Leu	Val	Glu	Lys	Gly	Ala	Ser	His	Ser	Phe
			95						100					105
Val	Ala	Glu	Ala	Lys	Pro	Pro	Thr	Val	Thr	Met	Pro	Arg	Ile	Lys
			110						115					120
Ala	Leu	Met	Thr	Gly	Ser	Leu	Pro	Gly	Phe	Val	Asp	Val	Ile	Arg
			125						130					135
Asn	Leu	Asn	Ser	Pro	Ala	Leu	Leu	Glu	Asp	Ser	Val	Ile	Arg	Gln
			140						145					150
Ala	Lys	Ala	Ala	Gly	Lys	Arg	Ile	Val	Phe	Tyr	Gly	Asp	Glu	Thr
			155						160					165
Trp	Val	Lys	Leu	Phe	Pro	Lys	His	Phe	Val	Glu	Tyr	Asp	Gly	Thr
			170						175					180

Thr	Ser	Phe	Phe	Val	Ser	Asp	Tyr	Thr	Glu	Val	Asp	Asn	Asn	Val
				185					190					195
Thr	Arg	His	Leu	Asp	Lys	Val	Leu	Lys	Arg	Gly	Asp	Trp	Asp	Ile
				200					205					210
Leu	Ile	Leu	His	Tyr	Leu	Gly	Leu	Asp	His	Ile	Gly	His	Ile	Ser
				215					220					225
Gly	Pro	Asn	Ser	Pro	Leu	Ile	Gly	Gln	Lys	Leu	Ser	Glu	Met	Asp
				230					235					240
Ser	Val	Leu	Met	Lys	Ile	His	Thr	Ser	Leu	Gln	Ser	Lys	Glu	Arg
				245					250					255
Glu	Thr	Pro	Leu	Pro	Asn	Leu	Leu	Val	Leu	Cys	Gly	Asp	His	Gly
				260					265					270
Met	Ser	Glu	Thr	Gly	Ser	His	Gly	Ala	Ser	Ser	Thr	Glu	Glu	Val
				275					280					285
Asn	Thr	Pro	Leu	Ile	Leu	Ile	Ser	Ser	Ala	Phe	Glu	Arg	Lys	Pro
				290					295					300
Gly	Asp	Ile	Arg	His	Pro	Lys	His	Val	Gln					
				305					310					

<210> 46

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 46

cgggactttc gctacctgtt gc 22

<210> 47

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 47

catcatattc cacaaaatgc ttgagg 26

<210> 48

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 48

ccttcgggga ttcttcccg cccccgttcg ttctctcg 38

<210> 49

<211> 918

<212> DNA

<213> Homo Sapien

<400> 49

agccaggcag cacatcacag cgggaggagc tgtcccaggt ggcccagctc 50
agcaatggca atgggggtcc ccagagtcac tctgctctgc ctctttgggg 100
ctgcgctctg cctgacaggg tcccaagccc tgcagtgcta cagctttgag 150
cacacctact ttggcccctt tgacctcagg gccatgaagc tgcccagcat 200
ctcctgtcct catgagtgtt ttgaggctat cctgtctctg gacaccgggt 250
atcgcgcgcc ggtgacctg gtgcggaagg gctgctggac cgggcctcct 300
gcgggccaga cgcaatcgaa cccggacgag ctgccgccag actactcggc 350
ggtgcgcggc tgcacaactg acaaatgcaa cgcccacctc atgactcatg 400
acgcctccc caacctgagc caagcaccg acccgccgac gctcagcggc 450
gccgagtgtc acgcctgtat cgggggtccac caggatgact gcgctatcgg 500
caggccccga cgagtccagt gtcaccagga ccagaccgcc tgcttccagg 550
gcagtggcag aatgacagtt ggcaatttct cagtccctgt gtacatcaga 600
acctgccacc ggccctcctg caccaccgag ggcaccacca gccctggac 650
agccatcgac ctccagggt cctgctgtga ggggtacctc tgcaacagga 700
aatccatgac ccagcccttc accagtgtt cagccaccac cctccccga 750
gcactacagg tcttgccct gctcctccca gtcctcctgc tgggtggggc 800
ctcagcatag accgcccctc caggatgtg gggacagggc tcacacacct 850
cattcttgct gcttcagccc ctatcacata gctcactgga aaatgatgtt 900
aaagtaagaa ttgcaaaa 918

<210> 50

<211> 251

<212> PRT

<213> Homo Sapien

<400> 50

Met	Ala	Met	Gly	Val	Pro	Arg	Val	Ile	Leu	Leu	Cys	Leu	Phe	Gly
1				5				10					15	
Ala	Ala	Leu	Cys	Leu	Thr	Gly	Ser	Gln	Ala	Leu	Gln	Cys	Tyr	Ser
				20				25					30	

Phe	Glu	His	Thr	Tyr	Phe	Gly	Pro	Phe	Asp	Leu	Arg	Ala	Met	Lys	35	40	45
Leu	Pro	Ser	Ile	Ser	Cys	Pro	His	Glu	Cys	Phe	Glu	Ala	Ile	Leu	50	55	60
Ser	Leu	Asp	Thr	Gly	Tyr	Arg	Ala	Pro	Val	Thr	Leu	Val	Arg	Lys	65	70	75
Gly	Cys	Trp	Thr	Gly	Pro	Pro	Ala	Gly	Gln	Thr	Gln	Ser	Asn	Pro	80	85	90
Asp	Ala	Leu	Pro	Pro	Asp	Tyr	Ser	Val	Val	Arg	Gly	Cys	Thr	Thr	95	100	105
Asp	Lys	Cys	Asn	Ala	His	Leu	Met	Thr	His	Asp	Ala	Leu	Pro	Asn	110	115	120
Leu	Ser	Gln	Ala	Pro	Asp	Pro	Pro	Thr	Leu	Ser	Gly	Ala	Glu	Cys	125	130	135
Tyr	Ala	Cys	Ile	Gly	Val	His	Gln	Asp	Asp	Cys	Ala	Ile	Gly	Arg	140	145	150
Ser	Arg	Arg	Val	Gln	Cys	His	Gln	Asp	Gln	Thr	Ala	Cys	Phe	Gln	155	160	165
Gly	Ser	Gly	Arg	Met	Thr	Val	Gly	Asn	Phe	Ser	Val	Pro	Val	Tyr	170	175	180
Ile	Arg	Thr	Cys	His	Arg	Pro	Ser	Cys	Thr	Thr	Glu	Gly	Thr	Thr	185	190	195
Ser	Pro	Trp	Thr	Ala	Ile	Asp	Leu	Gln	Gly	Ser	Cys	Cys	Glu	Gly	200	205	210
Tyr	Leu	Cys	Asn	Arg	Lys	Ser	Met	Thr	Gln	Pro	Phe	Thr	Ser	Ala	215	220	225
Ser	Ala	Thr	Thr	Pro	Pro	Arg	Ala	Leu	Gln	Val	Leu	Ala	Leu	Leu	230	235	240
Leu	Pro	Val	Leu	Leu	Leu	Val	Gly	Leu	Ser	Ala					245	250	

<210> 51
 <211> 3288
 <212> DNA
 <213> Homo Sapien

<400> 51
 cccacgcgctc cgggacagat gaacttaaaa gagaagcttt agctgccaaa 50
 gattgggaaa gggaaaggac aaaaaagacc cctgggctac acggcgtagg 100
 tgcagggttt cctactgctg ttcttttatg ctgggagctg tggctgtaac 150
 caactaggaa ataacgtatg cagcagctat ggctgtcaga gagttgtgct 200

ccttagttta tataacttatt attttatctt taagcatgct acttttactt 3150
 ggccaatatt ttcttatggt aacttttgct gatgtataaa acagactatg 3200
 ccttataatt gaaataaaat tataatctgc ctgaaaatga ataaaaataa 3250
 aacattttga aatgtgaaaa aaaaaaaaaa aaaaaaaaaa 3288

<210> 52
 <211> 800
 <212> PRT
 <213> Homo Sapien

<400> 52
 Met Ala Val Arg Glu Leu Cys Phe Pro Arg Gln Arg Gln Val Leu
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 20 25 30
 Gly Arg Tyr Ser Val Thr Glu Glu Thr Glu Lys Gly Ser Phe Val
 35 40 45
 Val Asn Leu Ala Lys Asp Leu Gly Leu Ala Glu Gly Glu Leu Ala
 50 55 60
 Ala Arg Gly Thr Arg Val Val Ser Asp Asp Asn Lys Gln Tyr Leu
 65 70 75
 Leu Leu Asp Ser His Thr Gly Asn Leu Leu Thr Asn Glu Lys Leu
 80 85 90
 Asp Arg Glu Lys Leu Cys Gly Pro Lys Glu Pro Cys Met Leu Tyr
 95 100 105
 Phe Gln Ile Leu Met Asp Asp Pro Phe Gln Ile Tyr Arg Ala Glu
 110 115 120
 Leu Arg Val Arg Asp Ile Asn Asp His Ala Pro Val Phe Gln Asp
 125 130 135
 Lys Glu Thr Val Leu Lys Ile Ser Glu Asn Thr Ala Glu Gly Thr
 140 145 150
 Ala Phe Arg Leu Glu Arg Ala Gln Asp Pro Asp Gly Gly Leu Asn
 155 160 165
 Gly Ile Gln Asn Tyr Thr Ile Ser Pro Asn Ser Phe Phe His Ile
 170 175 180
 Asn Ile Ser Gly Gly Asp Glu Gly Met Ile Tyr Pro Glu Leu Val
 185 190 195
 Leu Asp Lys Ala Leu Asp Arg Glu Glu Gln Gly Glu Leu Ser Leu
 200 205 210
 Thr Leu Thr Ala Leu Asp Gly Gly Ser Pro Ser Arg Ser Gly Thr
 215 220 225

Ser Thr Val Arg	Ile Val Val Leu Asp	Val Asn Asp Asn Ala Pro
230	235	240
Gln Phe Ala Gln	Ala Leu Tyr Glu Thr	Gln Ala Pro Glu Asn Ser
245	250	255
Pro Ile Gly Phe	Leu Ile Val Lys Val	Trp Ala Glu Asp Val Asp
260	265	270
Ser Gly Val Asn	Ala Glu Val Ser Tyr	Ser Phe Phe Asp Ala Ser
275	280	285
Glu Asn Ile Arg	Thr Thr Phe Gln Ile	Asn Pro Phe Ser Gly Glu
290	295	300
Ile Phe Leu Arg	Glu Leu Leu Asp Tyr	Glu Leu Val Asn Ser Tyr
305	310	315
Lys Ile Asn Ile	Gln Ala Met Asp Gly	Gly Gly Leu Ser Ala Arg
320	325	330
Cys Arg Val Leu	Val Glu Val Leu Asp	Thr Asn Asp Asn Pro Pro
335	340	345
Glu Leu Ile Val	Ser Ser Phe Ser Asn	Ser Val Ala Glu Asn Ser
350	355	360
Pro Glu Thr Pro	Leu Ala Val Phe Lys	Ile Asn Asp Arg Asp Ser
365	370	375
Gly Glu Asn Gly	Lys Met Val Cys Tyr	Ile Gln Glu Asn Leu Pro
380	385	390
Phe Leu Leu Lys	Pro Ser Val Glu Asn	Phe Tyr Ile Leu Ile Thr
395	400	405
Glu Gly Ala Leu	Asp Arg Glu Ile Arg	Ala Glu Tyr Asn Ile Thr
410	415	420
Ile Thr Val Thr	Asp Leu Gly Thr Pro	Arg Leu Lys Thr Glu His
425	430	435
Asn Ile Thr Val	Leu Val Ser Asp Val	Asn Asp Asn Ala Pro Ala
440	445	450
Phe Thr Gln Thr	Ser Tyr Thr Leu Phe	Val Arg Glu Asn Asn Ser
455	460	465
Pro Ala Leu His	Ile Gly Ser Val Ser	Ala Thr Asp Arg Asp Ser
470	475	480
Gly Thr Asn Ala	Gln Val Thr Tyr Ser	Leu Leu Pro Pro Gln Asp
485	490	495
Pro His Leu Pro	Leu Ala Ser Leu Val	Ser Ile Asn Ala Asp Asn
500	505	510
Gly His Leu Phe	Ala Leu Arg Ser Leu	Asp Tyr Glu Ala Leu Gln

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Ala Phe Glu Phe Arg Val Gly Ala Thr	Asp Arg Gly Ser Pro Ala	515	520	525
530	535			540
Leu Ser Arg Glu Ala Leu Val Arg Val	Leu Val Leu Asp Ala Asn			
545	550			555
Asp Asn Ser Pro Phe Val Leu Tyr Pro	Leu Gln Asn Gly Ser Ala			
560	565			570
Pro Cys Thr Glu Leu Val Pro Arg Ala	Ala Glu Pro Gly Tyr Leu			
575	580			585
Val Thr Lys Val Val Ala Val Asp Gly	Asp Ser Gly Gln Asn Ala			
590	595			600
Trp Leu Ser Tyr Gln Leu Leu Lys Ala	Thr Glu Pro Gly Leu Phe			
605	610			615
Gly Val Trp Ala His Asn Gly Glu Val	Arg Thr Ala Arg Leu Leu			
620	625			630
Ser Glu Arg Asp Ala Ala Lys His Arg	Leu Val Val Leu Val Lys			
635	640			645
Asp Asn Gly Glu Pro Pro Arg Ser Ala	Thr Ala Thr Leu His Leu			
650	655			660
Leu Leu Val Asp Gly Phe Ser Gln Pro	Tyr Leu Pro Leu Pro Glu			
665	670			675
Ala Ala Pro Ala Gln Ala Gln Ala Glu	Ala Asp Leu Leu Thr Val			
680	685			690
Tyr Leu Val Val Ala Leu Ala Ser Val	Ser Ser Leu Phe Leu Leu			
695	700			705
Ser Val Leu Leu Phe Val Ala Val Arg	Leu Cys Arg Arg Ser Arg			
710	715			720
Ala Ala Ser Val Gly Arg Cys Ser Val	Pro Glu Gly Pro Phe Pro			
725	730			735
Gly His Leu Val Asp Val Arg Gly Ala	Glu Thr Leu Ser Gln Ser			
740	745			750
Tyr Gln Tyr Glu Val Cys Leu Thr Gly	Gly Pro Gly Thr Ser Glu			
755	760			765
Phe Lys Phe Leu Lys Pro Val Ile Ser	Asp Ile Gln Ala Gln Gly			
770	775			780
Pro Gly Arg Lys Gly Glu Glu Asn Ser	Thr Phe Arg Asn Ser Phe			
785	790			795
Gly Phe Asn Ile Gln				
800				

<210> 53
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 53
ctggggagtg tccttggcag gttc 24

<210> 54
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 54
cagcatcacg ggctcttttag ggcacac 27

<210> 55
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 55
cgggtgactga ggaaacagag aaaggatcct ttgtggtcaa tctggc 46

<210> 56
<211> 2242
<212> DNA
<213> Homo Sapien

<220>
<221> unsure
<222> 2181
<223> unknown base

<400> 56
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tataccagcc tcgtcttctt tccgggggac aacgtgggctc agggcacaga 100
gagatattta atgtcaccct cttgggggctt tcatgggact ccctctgcca 150
catttttttg aggttgggaa agttgctaga ggcttcagaa ctccagccta 200
atggatccca aactcgggag aatggctgctg tccctgctgg ctgtgctgct 250
gctgctgctg gagecgggca tgttctctct accctccccg cccccggcgc 300
tgtttagagaa agtcttccag tacattgacc tccatcagga tgaatttgct 350


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aaatatccag agaatttggg tctagtatag tacattttcc cttccattta 1850
aaatgtcttg ggatatctgg atcagtaata aaatatttca aaggcacaga 1900
tggttgaaat ggtttaaggt cccccactgc acaccttcct caagtcatag 1950
ctgcttgacg caacttgatt tccccaaagtc ctgtgcaata gcccaggat 2000
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atcattccat ccaatgatcg cctttgcttt accactcttt ccttttatct 2150
tattaataaa aatgttggtc tccaccactg nctcccaaaa aaaaaaaaaa 2200
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 2242

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<210> 57

<211> 507

<212> PRT

<213> Homo Sapien

<400> 57

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Met Asp Pro Lys Leu Gly Arg Met Ala Ala Ser Leu Leu Ala Val
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Leu Leu Leu Leu Leu Glu Arg Gly Met Phe Ser Ser Pro Ser Pro
          20          25          30
Pro Pro Ala Leu Leu Glu Lys Val Phe Gln Tyr Ile Asp Leu His
          35          40          45
Gln Asp Glu Phe Val Gln Thr Leu Lys Glu Trp Val Ala Ile Glu
          50          55          60
Ser Asp Ser Val Gln Pro Val Pro Arg Phe Arg Gln Glu Leu Phe
          65          70          75
Arg Met Met Ala Val Ala Ala Asp Thr Leu Gln Arg Leu Gly Ala
          80          85          90
Arg Val Ala Ser Val Asp Met Gly Pro Gln Gln Leu Pro Asp Gly
          95          100          105
Gln Ser Leu Pro Ile Pro Pro Val Ile Leu Ala Glu Leu Gly Ser
          110          115          120
Asp Pro Thr Lys Gly Thr Val Cys Phe Tyr Gly His Leu Asp Val
          125          130          135
Gln Pro Ala Asp Arg Gly Asp Gly Trp Leu Thr Asp Pro Tyr Val
          140          145          150
Leu Thr Glu Val Asp Gly Lys Leu Tyr Gly Arg Gly Ala Thr Asp
          155          160          165
Asn Lys Gly Pro Val Leu Ala Trp Ile Asn Ala Val Ser Ala Phe

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170 175 180
 Arg Ala Leu Glu Gln Asp Leu Pro Val Asn Ile Lys Phe Ile Ile
 185 190 195
 Glu Gly Met Glu Glu Ala Gly Ser Val Ala Leu Glu Glu Leu Val
 200 205 210
 Glu Lys Glu Lys Asp Arg Phe Phe Ser Gly Val Asp Tyr Ile Val
 215 220 225
 Ile Ser Asp Asn Leu Trp Ile Ser Gln Arg Lys Pro Ala Ile Thr
 230 235 240
 Tyr Gly Thr Arg Gly Asn Ser Tyr Phe Met Val Glu Val Lys Cys
 245 250 255
 Arg Asp Gln Asp Phe His Ser Gly Thr Phe Gly Gly Ile Leu His
 260 265 270
 Glu Pro Met Ala Asp Leu Val Ala Leu Leu Gly Ser Leu Val Asp
 275 280 285
 Ser Ser Gly His Ile Leu Val Pro Gly Ile Tyr Asp Glu Val Val
 290 295 300
 Pro Leu Thr Glu Glu Glu Ile Asn Thr Tyr Lys Ala Ile His Leu
 305 310 315
 Asp Leu Glu Glu Tyr Arg Asn Ser Ser Arg Val Glu Lys Phe Leu
 320 325 330
 Phe Asp Thr Lys Glu Glu Ile Leu Met His Leu Trp Arg Tyr Pro
 335 340 345
 Ser Leu Ser Ile His Gly Ile Glu Gly Ala Phe Asp Glu Pro Gly
 350 355 360
 Thr Lys Thr Val Ile Pro Gly Arg Val Ile Gly Lys Phe Ser Ile
 365 370 375
 Arg Leu Val Pro His Met Asn Val Ser Ala Val Glu Lys Gln Val
 380 385 390
 Thr Arg His Leu Glu Asp Val Phe Ser Lys Arg Asn Ser Ser Asn
 395 400 405
 Lys Met Val Val Ser Met Thr Leu Gly Leu His Pro Trp Ile Ala
 410 415 420
 Asn Ile Asp Asp Thr Gln Tyr Leu Ala Ala Lys Arg Ala Ile Arg
 425 430 435
 Thr Val Phe Gly Thr Glu Pro Asp Met Ile Arg Asp Gly Ser Thr
 440 445 450
 Ile Pro Ile Ala Lys Met Phe Gln Glu Ile Val His Lys Ser Val
 455 460 465

170 175 180
 Arg Ala Leu Glu Gln Asp Leu Pro Val Asn Ile Lys Phe Ile Ile
 185 190 195
 Glu Gly Met Glu Glu Ala Gly Ser Val Ala Leu Glu Glu Leu Val
 200 205 210
 Glu Lys Glu Lys Asp Arg Phe Phe Ser Gly Val Asp Tyr Ile Val
 215 220 225
 Ile Ser Asp Asn Leu Trp Ile Ser Gln Arg Lys Pro Ala Ile Thr
 230 235 240
 Tyr Gly Thr Arg Gly Asn Ser Tyr Phe Met Val Glu Val Lys Cys
 245 250 255
 Arg Asp Gln Asp Phe His Ser Gly Thr Phe Gly Gly Ile Leu His
 260 265 270
 Glu Pro Met Ala Asp Leu Val Ala Leu Leu Gly Ser Leu Val Asp
 275 280 285
 Ser Ser Gly His Ile Leu Val Pro Gly Ile Tyr Asp Glu Val Val
 290 295 300
 Pro Leu Thr Glu Glu Glu Ile Asn Thr Tyr Lys Ala Ile His Leu
 305 310 315
 Asp Leu Glu Glu Tyr Arg Asn Ser Ser Arg Val Glu Lys Phe Leu
 320 325 330
 Phe Asp Thr Lys Glu Glu Ile Leu Met His Leu Trp Arg Tyr Pro
 335 340 345
 Ser Leu Ser Ile His Gly Ile Glu Gly Ala Phe Asp Glu Pro Gly
 350 355 360
 Thr Lys Thr Val Ile Pro Gly Arg Val Ile Gly Lys Phe Ser Ile
 365 370 375
 Arg Leu Val Pro His Met Asn Val Ser Ala Val Glu Lys Gln Val
 380 385 390
 Thr Arg His Leu Glu Asp Val Phe Ser Lys Arg Asn Ser Ser Asn
 395 400 405
 Lys Met Val Val Ser Met Thr Leu Gly Leu His Pro Trp Ile Ala
 410 415 420
 Asn Ile Asp Asp Thr Gln Tyr Leu Ala Ala Lys Arg Ala Ile Arg
 425 430 435
 Thr Val Phe Gly Thr Glu Pro Asp Met Ile Arg Asp Gly Ser Thr
 440 445 450
 Ile Pro Ile Ala Lys Met Phe Gln Glu Ile Val His Lys Ser Val
 455 460 465

Val	Leu	Ile	Pro	Leu	Gly	Ala	Val	Asp	Asp	Gly	Glu	His	Ser	Gln
				470					475					480
Asn	Glu	Lys	Ile	Asn	Arg	Trp	Asn	Tyr	Ile	Glu	Gly	Thr	Lys	Leu
				485					490					495
Phe	Ala	Ala	Phe	Phe	Leu	Glu	Met	Ala	Gln	Leu	His			
				500					505					

<210> 58
 <211> 1470
 <212> DNA
 <213> Homo Sapien

<400> 58
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 acactacctt cccgaagttg aaggcaagcg gtgattgttt gtagacggcg 100
 ctttgtcatg ggacctgtgc ggttggaat attgcttttc ctttttttg 150
 ccgtgcacga ggcttgggct gggatgttga aggaggagga cgatgacaca 200
 gaacgcttgc ccagcaaagt cgaagtgtgt aagctgctga gcacagagct 250
 acaggcggaa ctgagtcgca ccggtcgatc tcgagaggtg ctggagctgg 300
 ggcaggtgct ggatacagga aagaggaaga gacacgtgcc ttacagcgtt 350
 tcagagacaa ggctggaaga ggccttagag aatttatgtg agcggatcct 400
 ggactatagt gttcacgctg agcgcaaggg ctcactgaga tatgccaagg 450
 gtcagagtca gaccatggca aactgaaag gcctagtga gaaggggggtg 500
 aaggtggatc tggggatccc tctggagctt tgggatgagc ccagcgtgga 550
 ggtcacatac ctcaagaagc agtgtgagac catgttggag gagtttgaag 600
 acattgtggg agactgggtac ttccaccatc aggagcagcc cctacaaaat 650
 tttctctgtg aaggtcatgt gctcccagct gctgaaactg catgtctaca 700
 ggaaacttgg actggaaagg agatcacaga tggggaagag aaaacagaag 750
 gggaggaaga gcaggaggag gaggaggaag aggaggaaga ggaaggggga 800
 gacaagatga ccaagacagg aagccacccc aaacttgacc gagaagatct 850
 ttgacccttg cctttgagcc ccaggaggg gaagggatca tggagagccc 900
 tctaaagcct gcactctccc tgctccacag ctttcagggt gtgtttatga 950
 gtgactccac ccaagcttgt agctgttctc tcccatctaa cctcaggcaa 1000
 gatcctggtg aaacagcatg acatggcttc tggggtggag ggtgggggtg 1050
 gaggtcctgc tcctagagat gaactctatc cagccctta attggcaggt 1100

gtatgtgctg acagtactga aagctttcct ctttaactga tcccaccccc 1150
 acccaaaagt cagcagtggc actggagctg tgggctttgg ggaagtcact 1200
 tagctcctta aggtctgttt ttagaccctt ccaaggaaga ggccagaacg 1250
 gacattctct gcgatctata tacattgcct gtatccagga ggctacacac 1300
 cagcaaaccg tgaaggagaa tgggacactg ggtcatggcc tggagttgct 1350
 gataatttag gtgggataga tacttgggtct acttaagctc aatgtaaccc 1400
 agagcccacc atatagtttt ataggtgctc aactttctat atcgctatta 1450
 aacttttttc tttttttcta 1470

<210> 59

<211> 248

<212> PRT

<213> Homo Sapien

<400> 59

Met	Gly	Pro	Val	Arg	Leu	Gly	Ile	Leu	Leu	Phe	Leu	Phe	Leu	Ala
1				5				10						15
Val	His	Glu	Ala	Trp	Ala	Gly	Met	Leu	Lys	Glu	Glu	Asp	Asp	Asp
				20				25						30
Thr	Glu	Arg	Leu	Pro	Ser	Lys	Cys	Glu	Val	Cys	Lys	Leu	Leu	Ser
				35				40						45
Thr	Glu	Leu	Gln	Ala	Glu	Leu	Ser	Arg	Thr	Gly	Arg	Ser	Arg	Glu
				50				55						60
Val	Leu	Glu	Leu	Gly	Gln	Val	Leu	Asp	Thr	Gly	Lys	Arg	Lys	Arg
				65				70						75
His	Val	Pro	Tyr	Ser	Val	Ser	Glu	Thr	Arg	Leu	Glu	Glu	Ala	Leu
				80				85						90
Glu	Asn	Leu	Cys	Glu	Arg	Ile	Leu	Asp	Tyr	Ser	Val	His	Ala	Glu
				95				100						105
Arg	Lys	Gly	Ser	Leu	Arg	Tyr	Ala	Lys	Gly	Gln	Ser	Gln	Thr	Met
				110				115						120
Ala	Thr	Leu	Lys	Gly	Leu	Val	Gln	Lys	Gly	Val	Lys	Val	Asp	Leu
				125				130						135
Gly	Ile	Pro	Leu	Glu	Leu	Trp	Asp	Glu	Pro	Ser	Val	Glu	Val	Thr
				140				145						150
Tyr	Leu	Lys	Lys	Gln	Cys	Glu	Thr	Met	Leu	Glu	Glu	Phe	Glu	Asp
				155				160						165
Ile	Val	Gly	Asp	Trp	Tyr	Phe	His	His	Gln	Glu	Gln	Pro	Leu	Gln
				170				175						180

Asn	Phe	Leu	Cys	Glu	Gly	His	Val	Leu	Pro	Ala	Ala	Glu	Thr	Ala
				185					190					195
Cys	Leu	Gln	Glu	Thr	Trp	Thr	Gly	Lys	Glu	Ile	Thr	Asp	Gly	Glu
				200					205					210
Glu	Lys	Thr	Glu	Gly	Glu	Glu	Glu	Gln	Glu	Glu	Glu	Glu	Glu	Glu
				215					220					225
Glu	Glu	Glu	Glu	Gly	Gly	Asp	Lys	Met	Thr	Lys	Thr	Gly	Ser	His
				230					235					240
Pro	Lys	Leu	Asp	Arg	Glu	Asp	Leu							
				245										

<210> 60
 <211> 890
 <212> DNA
 <213> Homo Sapien

<400> 60
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 atgaggctgg tcacagcagc actgttactg ggtctcatga tgggtggtcac 150
 tggagacgag gatgagaaca gcccgtgtgc ccatgaggcc ctcttggtacg 200
 aggacaccct cttttgccag ggccttgaag ttttctaccc agagttgggg 250
 aacattggct gcaaggttgt tcttgattgt aacaactaca gacagaagat 300
 cacctcctgg atggagccga tagtcaagtt cccggggggc gtggacggcg 350
 caacctatat cctggtgatg gtggatccag atgccctag cagagcagaa 400
 cccagacaga gattctggag acattggctg gtaacagata tcaagggcgc 450
 cgacctgaag aaagggaaga ttcagggcca ggagttatca gcctaccagg 500
 ctccctcccc accggcacac agtggcttcc atcgctacca gttctttgtc 550
 tatcttcagg aaggaaaagt catctctctc cttcccaagg aaaacaaaac 600
 tcgaggctct tggaaaatgg acagatttct gaaccgcttc cacctgggcg 650
 aacctgaagc aagcaccacag ttcattgaccc agaactacca ggactcacca 700
 accctccagg ctcccagagg aaggggccagc gagcccaagc acaaaaccag 750
 gcagagatag ctgcctgcta gatagccggc tttgccatcc gggcatgtgg 800
 ccacactgct caccaccgac gatgtgggta tggaaccccc tctggatata 850
 gaacccttc ttttccaaat taaaaaaaaa aatcatcaaa 890

<210> 61

<211> 223
 <212> PRT
 <213> Homo Sapien

<400> 61

Met	Gly	Trp	Thr	Met	Arg	Leu	Val	Thr	Ala	Ala	Leu	Leu	Leu	Gly	1	5	10	15
Leu	Met	Met	Val	Val	Thr	Gly	Asp	Glu	Asp	Glu	Asn	Ser	Pro	Cys	20	25	30	
Ala	His	Glu	Ala	Leu	Leu	Asp	Glu	Asp	Thr	Leu	Phe	Cys	Gln	Gly	35	40	45	
Leu	Glu	Val	Phe	Tyr	Pro	Glu	Leu	Gly	Asn	Ile	Gly	Cys	Lys	Val	50	55	60	
Val	Pro	Asp	Cys	Asn	Asn	Tyr	Arg	Gln	Lys	Ile	Thr	Ser	Trp	Met	65	70	75	
Glu	Pro	Ile	Val	Lys	Phe	Pro	Gly	Ala	Val	Asp	Gly	Ala	Thr	Tyr	80	85	90	
Ile	Leu	Val	Met	Val	Asp	Pro	Asp	Ala	Pro	Ser	Arg	Ala	Glu	Pro	95	100	105	
Arg	Gln	Arg	Phe	Trp	Arg	His	Trp	Leu	Val	Thr	Asp	Ile	Lys	Gly	110	115	120	
Ala	Asp	Leu	Lys	Lys	Gly	Lys	Ile	Gln	Gly	Gln	Glu	Leu	Ser	Ala	125	130	135	
Tyr	Gln	Ala	Pro	Ser	Pro	Pro	Ala	His	Ser	Gly	Phe	His	Arg	Tyr	140	145	150	
Gln	Phe	Phe	Val	Tyr	Leu	Gln	Glu	Gly	Lys	Val	Ile	Ser	Leu	Leu	155	160	165	
Pro	Lys	Glu	Asn	Lys	Thr	Arg	Gly	Ser	Trp	Lys	Met	Asp	Arg	Phe	170	175	180	
Leu	Asn	Arg	Phe	His	Leu	Gly	Glu	Pro	Glu	Ala	Ser	Thr	Gln	Phe	185	190	195	
Met	Thr	Gln	Asn	Tyr	Gln	Asp	Ser	Pro	Thr	Leu	Gln	Ala	Pro	Arg	200	205	210	
Gly	Arg	Ala	Ser	Glu	Pro	Lys	His	Lys	Thr	Arg	Gln	Arg	215	220				

<210> 62
 <211> 1321
 <212> DNA
 <213> Homo Sapien

<400> 62

gtcgacccac gcgtccgaag ctgctggagc caccgattcag tcccctggac 50

tgtagataaa gaccctttct tgccagggtgc tgagacaacc acactatgag 100
 aggcactcca ggagacgctg atgggtggagg aagggccgtc tatcaatcaa 150
 tcaactgttgc tgttatcaca tgcaagtatc cagaggctct tgagcaaggc 200
 agaggggatc ccattttattt gggaatccag aatccagaaa tgtgtttgta 250
 ttgtgagaag gttggagaac agcccacatt gcagctaaaa gagcagaaga 300
 tcatggatct gtatggccaa cccgagcccg tgaaaccctt ctttttctac 350
 cgtgccaaaga ctggtaggac ctccaccctt gagtctgtgg ctttcccgga 400
 ctggttcatt gcctcctcca agagagacca gcccatcatt ctgacttcag 450
 aacttgggaa gtcatacaac actgcctttg aattaaatat aaatgactga 500
 actcagccta gaggtggcag cttgggtcttt gtcttaaagt ttctgggtcc 550
 caatgtgttt tcgtctacat tttcttagtg tcattttcac gctggtgctg 600
 agacaggagc aaggctgctg ttatcatctc attttataat gaagaagaag 650
 caattacttc atagcaactg aagaacagga tgtggcctca gaagcaggag 700
 agctgggtgg tataaggctg tcctctcaag ctgggtgctgt gtaggccaca 750
 aggcattctgc atgagtgact ttaagactca aagaccaaac actgagcttt 800
 cttctagggg tgggtatgaa gatgcttcag agctcatgcg cgttaccac 850
 gatggcatga ctagcacaga gctgatctct gtttctgttt tgctttattc 900
 cctcttggga tgatatcatc cagtctttat atgttgccaa tatacctcat 950
 tgtgtgtaat agaaccttct tagcatlaag accttgtaaa caaaaataat 1000
 tcttgggggtg ggtatgaaga tgcttcagag ctcatgcgcg ttaccacga 1050
 tggcatgact agcacagagc tgatctctgt ttctgttttg ctttattccc 1100
 tcttgggatg atatcatcca gtctttatat gttgccaata tacctcattg 1150
 tgtgtaatag aaccttctta gcattaagac cttgtaaaca aaaataattc 1200
 ttgtgttaag ttaaatcatt tttgtcctaa ttgtaatgtg taatcttaaa 1250
 gttaaataaa ctttgtgtat ttatataata ataaagctaa aactgatata 1300
 aaataaagaa agagtaaact g 1321

<210> 63
 <211> 134
 <212> PRT
 <213> Homo Sapien

 <400> 63

Met	Arg	Gly	Thr	Pro	Gly	Asp	Ala	Asp	Gly	Gly	Gly	Arg	Ala	Val	1	5	10	15
Tyr	Gln	Ser	Ile	Thr	Val	Ala	Val	Ile	Thr	Cys	Lys	Tyr	Pro	Glu	20	25	30	
Ala	Leu	Glu	Gln	Gly	Arg	Gly	Asp	Pro	Ile	Tyr	Leu	Gly	Ile	Gln	35	40	45	
Asn	Pro	Glu	Met	Cys	Leu	Tyr	Cys	Glu	Lys	Val	Gly	Glu	Gln	Pro	50	55	60	
Thr	Leu	Gln	Leu	Lys	Glu	Gln	Lys	Ile	Met	Asp	Leu	Tyr	Gly	Gln	65	70	75	
Pro	Glu	Pro	Val	Lys	Pro	Phe	Leu	Phe	Tyr	Arg	Ala	Lys	Thr	Gly	80	85	90	
Arg	Thr	Ser	Thr	Leu	Glu	Ser	Val	Ala	Phe	Pro	Asp	Trp	Phe	Ile	95	100	105	
Ala	Ser	Ser	Lys	Arg	Asp	Gln	Pro	Ile	Ile	Leu	Thr	Ser	Glu	Leu	110	115	120	
Gly	Lys	Ser	Tyr	Asn	Thr	Ala	Phe	Glu	Leu	Asn	Ile	Asn	Asp	125	130			

<210> 64
 <211> 999
 <212> DNA
 <213> Homo Sapien

<400> 64
 gcgaggctgc accagcgcct ggcaccatga ggacgcctgg gcctctgccc 50
 gtgctgctgc tgctcctggc gggagccccc gccgcgcggc ccactcccc 100
 gacctgctac tcccgcacgc gggccctgag ccaggagatc acccgcgact 150
 tcaacctcct gcaggtctcg gagccctcgg agccatgtgt gagatacctg 200
 cccaggctgt acctggacat acacaattac tgtgtgctgg acaagctgcg 250
 ggactttgtg gcctcgcccc cgtgttgga agtgcccag gtagattcct 300
 tgaaggacaa agcacggaag ctgtacacca tcatgaactc gttctgcagg 350
 agagatttgg tattcctggt ggatgactgc aatgccttgg aatacccaat 400
 cccagtgact acggtcctgc cagatcgtca gcgctaagg aactgagacc 450
 agagaaagaa cccaagagaa ctaaagttat gtcagctacc cagacttaat 500
 gggccagagc catgaccctc acaggtcttg tgtagttgt atctgaaact 550
 gttatgtatc tctctacctt ctggaaaaca gggctggtat tcctaccag 600
 gaacctcctt tgagcataga gttagcaacc atgcttctca ttcccttgac 650

tcattgtcttg ccaggatggg tagatacaca gcatgttgat ttggtcacta 700
 aaaagaagaa aaggactaac aagcttcact tttatgaaca actattttga 750
 gaacatgcac aatagtatgt ttttattact ggtttaatgg agtaatggta 800
 cttttattct ttcttgatag aaacctgctt acatttaacc aagcttctat 850
 tatgcctttt tctaacacag actttcttca ctgtctttca tttaaaaaga 900
 aattaatgct ctttaagatat atattttacg tagtgctgac aggacccact 950
 ctttcattga aagggtgatga aaatcaaata aagaatctct tcacatgga 999

<210> 65
 <211> 136
 <212> PRT
 <213> Homo Sapien

<400> 65
 Met Arg Thr Pro Gly Pro Leu Pro Val Leu Leu Leu Leu Leu Ala
 1 5 10 15
 Gly Ala Pro Ala Ala Arg Pro Thr Pro Pro Thr Cys Tyr Ser Arg
 20 25 30
 Met Arg Ala Leu Ser Gln Glu Ile Thr Arg Asp Phe Asn Leu Leu
 35 40 45
 Gln Val Ser Glu Pro Ser Glu Pro Cys Val Arg Tyr Leu Pro Arg
 50 55 60
 Leu Tyr Leu Asp Ile His Asn Tyr Cys Val Leu Asp Lys Leu Arg
 65 70 75
 Asp Phe Val Ala Ser Pro Pro Cys Trp Lys Val Ala Gln Val Asp
 80 85 90
 Ser Leu Lys Asp Lys Ala Arg Lys Leu Tyr Thr Ile Met Asn Ser
 95 100 105
 Phe Cys Arg Arg Asp Leu Val Phe Leu Leu Asp Asp Cys Asn Ala
 110 115 120
 Leu Glu Tyr Pro Ile Pro Val Thr Thr Val Leu Pro Asp Arg Gln
 125 130 135

Arg

<210> 66
 <211> 1893
 <212> DNA
 <213> Homo Sapien

<400> 66
 gtctccgcgt cacaggaact tcagcaccca cagggcggac agcgctcccc 50

tetacctgga gacttgactc ccgcgcgccc caacctgct tatcccttga 100
 ccgtcgagtg tcagagatcc tgcagccgcc cagtcccggc cctctctccg 150
 cccacacccc accctcctgg ctcttctgt ttttactcct ccttttcatt 200
 cataacaaaa gctacagctc caggagccca gcgccgggct gtgaccaag 250
 ccgagcgtgg aagaatgggg ttcctcgga ccggcacttg gattctggtg 300
 ttagtgctcc cgattcaagc tttcccaaaa cctggaggaa gccaaagaca 350
 atctctacat aatagagaat taagtgcaga aagaccttg aatgaacaga 400
 ttgctgaagc agaagaagac aagattaaaa aaacatatcc tccagaaaac 450
 aagccaggtc agagcaacta ttcttttggt gataactga acctgctaaa 500
 ggcaataaca gaaaaggaaa aaattgagaa agaaagaca tctataagaa 550
 gctcccact tgataataag ttgaatgtgg aagatgttga ttcaaccaag 600
 aatcgaaaaac tgatcgatga ttatgactct actaagagt gattggatca 650
 taaatttcaa gatgatccag atggtcttca tcaactagac gggactcctt 700
 taaccgctga agacattgtc cataaaatcg ctgccaggat ttatgaagaa 750
 aatgacagag ccgtgtttga caagattggt tctaaactac ttaatctcgg 800
 ccttatcaca gaaagccaag cacatacact ggaagatgaa gtagcagagg 850
 ttttacaaaa attaattctc aaggaagcca acaattatga ggaggatccc 900
 aataagccca caagctggac tgagaatcag gctggaaaaa taccagagaa 950
 agtgactcca atggcagcaa ttcaagatgg tcttgctaag ggagaaaacg 1000
 atgaaacagt atctaacaca ttaacctga caaatggctt ggaaaggaga 1050
 actaaaacct acagtgaaga caactttgag gaactccaat atttcccaa 1100
 tttctatgcg ctactgaaaa gtattgattc agaaaaagaa gcaaaagaga 1150
 aagaaacact gattactatc atgaaaacac tgattgactt tgtgaagatg 1200
 atggtgaaat atggaacaat atctccagaa gaaggtgttt cctaccttga 1250
 aaacttggat gaaatgattg ctcttcagac caaaaacaag ctagaaaaaa 1300
 atgctactga caatataagc aagcttttcc cagcaccatc agagaagagt 1350
 catgaagaaa cagacagtac caaggaagaa gcagctaaga tggaaaagga 1400
 atatggaagc ttgaaggatt ccacaaaaga tgataactcc aaccaggag 1450
 gaaagacaga tgaacccaaa ggaaaaacag aagcctatth ggaagccatc 1500

agaaaaaata ttgaatgggt gaagaaacat gacaaaaagg gaaataaaga 1550
 agattatgac ctttcaaaga tgagagactt catcaataaa caagctgatg 1600
 cttatgtgga gaaaggcatc cttgacaagg aagaagccga ggccatcaag 1650
 cgcatttata gcagcctgta aaaatggcaa aagatccagg agtctttcaa 1700
 ctgtttcaga aaacataata tagcttaaaa cactttcta tctgtgatta 1750
 aaatTTTTTg acccaaggggt tattagaaag tgctgaattt acagtagtta 1800
 accttttaca agtggtttaa acatagcttt cttcccgtaa aaactatctg 1850
 aaagtaaagt tgtatgtaag ctgaaaaaaaa aaaaaaaaaa aaa 1893

<210> 67

<211> 468

<212> PRT

<213> Homo Sapien

<400> 67

Met	Gly	Phe	Leu	Gly	Thr	Gly	Thr	Trp	Ile	Leu	Val	Leu	Val	Leu
1				5					10					15
Pro	Ile	Gln	Ala	Phe	Pro	Lys	Pro	Gly	Gly	Ser	Gln	Asp	Lys	Ser
				20					25					30
Leu	His	Asn	Arg	Glu	Leu	Ser	Ala	Glu	Arg	Pro	Leu	Asn	Glu	Gln
				35					40					45
Ile	Ala	Glu	Ala	Glu	Glu	Asp	Lys	Ile	Lys	Lys	Thr	Tyr	Pro	Pro
				50					55					60
Glu	Asn	Lys	Pro	Gly	Gln	Ser	Asn	Tyr	Ser	Phe	Val	Asp	Asn	Leu
				65					70					75
Asn	Leu	Leu	Lys	Ala	Ile	Thr	Glu	Lys	Glu	Lys	Ile	Glu	Lys	Glu
				80					85					90
Arg	Gln	Ser	Ile	Arg	Ser	Ser	Pro	Leu	Asp	Asn	Lys	Leu	Asn	Val
				95					100					105
Glu	Asp	Val	Asp	Ser	Thr	Lys	Asn	Arg	Lys	Leu	Ile	Asp	Asp	Tyr
				110					115					120
Asp	Ser	Thr	Lys	Ser	Gly	Leu	Asp	His	Lys	Phe	Gln	Asp	Asp	Pro
				125					130					135
Asp	Gly	Leu	His	Gln	Leu	Asp	Gly	Thr	Pro	Leu	Thr	Ala	Glu	Asp
				140					145					150
Ile	Val	His	Lys	Ile	Ala	Ala	Arg	Ile	Tyr	Glu	Glu	Asn	Asp	Arg
				155					160					165
Ala	Val	Phe	Asp	Lys	Ile	Val	Ser	Lys	Leu	Leu	Asn	Leu	Gly	Leu
				170					175					180

Ile Thr Glu Ser	Gln Ala His Thr Leu	Glu Asp Glu Val Ala Glu	185	190	195
Val Leu Gln Lys	Leu Ile Ser Lys Glu	Ala Asn Asn Tyr Glu Glu	200	205	210
Asp Pro Asn Lys	Pro Thr Ser Trp Thr	Glu Asn Gln Ala Gly Lys	215	220	225
Ile Pro Glu Lys	Val Thr Pro Met Ala	Ala Ile Gln Asp Gly Leu	230	235	240
Ala Lys Gly Glu	Asn Asp Glu Thr Val	Ser Asn Thr Leu Thr Leu	245	250	255
Thr Asn Gly Leu	Glu Arg Arg Thr Lys	Thr Tyr Ser Glu Asp Asn	260	265	270
Phe Glu Glu Leu	Gln Tyr Phe Pro Asn	Phe Tyr Ala Leu Leu Lys	275	280	285
Ser Ile Asp Ser	Glu Lys Glu Ala Lys	Glu Lys Glu Thr Leu Ile	290	295	300
Thr Ile Met Lys	Thr Leu Ile Asp Phe	Val Lys Met Met Val Lys	305	310	315
Tyr Gly Thr Ile	Ser Pro Glu Glu Gly	Val Ser Tyr Leu Glu Asn	320	325	330
Leu Asp Glu Met	Ile Ala Leu Gln Thr	Lys Asn Lys Leu Glu Lys	335	340	345
Asn Ala Thr Asp	Asn Ile Ser Lys Leu	Phe Pro Ala Pro Ser Glu	350	355	360
Lys Ser His Glu	Glu Thr Asp Ser Thr	Lys Glu Glu Ala Ala Lys	365	370	375
Met Glu Lys Glu	Tyr Gly Ser Leu Lys	Asp Ser Thr Lys Asp Asp	380	385	390
Asn Ser Asn Pro	Gly Gly Lys Thr Asp	Glu Pro Lys Gly Lys Thr	395	400	405
Glu Ala Tyr Leu	Glu Ala Ile Arg Lys	Asn Ile Glu Trp Leu Lys	410	415	420
Lys His Asp Lys	Lys Gly Asn Lys Glu	Asp Tyr Asp Leu Ser Lys	425	430	435
Met Arg Asp Phe	Ile Asn Lys Gln Ala	Asp Ala Tyr Val Glu Lys	440	445	450
Gly Ile Leu Asp	Lys Glu Glu Ala Glu	Ala Ile Lys Arg Ile Tyr	455	460	465
Ser Ser Leu					

<210> 68
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 68
cgtcacagga acttcagcac cc 22

<210> 69
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 69
gtcttggctt cctccaggtt tgg 23

<210> 70
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 70
ggacagcgct cccctctacc tggagacttg actcccgc 38

<210> 71
<211> 2379
<212> DNA
<213> Homo Sapien

<400> 71
gttgctccgg cggcgctcgg ggagggagcc agcagcctag ggcctaggcc 50
cgggccacca tggcgctgcc tccaggccca gccgccctcc ggcacacact 100
gctgctcctg ccagcccttc tgagctcagg ttggggggag ttggagccac 150
aaatagatgg tcagacctgg gctgagcggg cacttcggga gaatgaacgc 200
cacgccttca cctgccgggt ggcagggggg cctggcacc ccagattggc 250
ctggtatctg gatggacagc tgcaggaggc cagcacctca agactgctga 300
gcgtgggagg ggaggccttc tctggaggca ccagcacctt cactgtcact 350
gcccatcggg cccagcatga gctcaactgc tctctgcagg accccagaag 400
tggccgatca gccaacgcct ctgtcatcct taatgtgcaa ttcaagccag 450

tctgggattc actgtgagtg tcttgagctc tcgggggttg tggtttttct 1950
ctcagcatgt ctctccacc acgggacccc agccctgacc aacccatggt 2000
tgccatca gacaggaagg ggccttctg gaggatggc gccacaggca 2050
cataattcaa cagtgtggaa gctttagggg aacatggaga aagaaggaga 2100
ccacatcccc caaagtgacc taagaacact ttaaaaagca acatgtaaat 2150
gattggaaat taatatagta cagaatatat tttcccttg ttgagatctt 2200
cttttgtaat gtttttcatg ttactgccta gggcggtgct gagcacacag 2250
caagtttaat aaacttgact gaattcattt aaaaaaaaaa aaaaaaaaaa 2300
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2350
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2379

<210> 72
<211> 322
<212> PRT
<213> Homo Sapien

<400> 72
Met Ala Leu Pro Pro Gly Pro Ala Ala Leu Arg His Thr Leu Leu
1 5 10 15
Leu Leu Pro Ala Leu Leu Ser Ser Gly Trp Gly Glu Leu Glu Pro
20 25 30
Gln Ile Asp Gly Gln Thr Trp Ala Glu Arg Ala Leu Arg Glu Asn
35 40 45
Glu Arg His Ala Phe Thr Cys Arg Val Ala Gly Gly Pro Gly Thr
50 55 60
Pro Arg Leu Ala Trp Tyr Leu Asp Gly Gln Leu Gln Glu Ala Ser
65 70 75
Thr Ser Arg Leu Leu Ser Val Gly Gly Glu Ala Phe Ser Gly Gly
80 85 90
Thr Ser Thr Phe Thr Val Thr Ala His Arg Ala Gln His Glu Leu
95 100 105
Asn Cys Ser Leu Gln Asp Pro Arg Ser Gly Arg Ser Ala Asn Ala
110 115 120
Ser Val Ile Leu Asn Val Gln Phe Lys Pro Glu Ile Ala Gln Val
125 130 135
Gly Ala Lys Tyr Gln Glu Ala Gln Gly Pro Gly Leu Leu Val Val
140 145 150
Leu Phe Ala Leu Val Arg Ala Asn Pro Pro Ala Asn Val Thr Trp
155 160 165

Ile	Asp	Gln	Asp	Gly	Pro	Val	Thr	Val	Asn	Thr	Ser	Asp	Phe	Leu	
				170					175					180	
Val	Leu	Asp	Ala	Gln	Asn	Tyr	Pro	Trp	Leu	Thr	Asn	His	Thr	Val	
				185					190					195	
Gln	Leu	Gln	Leu	Arg	Ser	Leu	Ala	His	Asn	Leu	Ser	Val	Val	Ala	
				200					205					210	
Thr	Asn	Asp	Val	Gly	Val	Thr	Ser	Ala	Ser	Leu	Pro	Ala	Pro	Gly	
				215					220					225	
Pro	Ser	Arg	His	Pro	Ser	Leu	Ile	Ser	Ser	Asp	Ser	Asn	Asn	Leu	
				230					235					240	
Lys	Leu	Asn	Asn	Val	Arg	Leu	Pro	Arg	Glu	Asn	Met	Ser	Leu	Pro	
				245					250					255	
Ser	Asn	Leu	Gln	Leu	Asn	Asp	Leu	Thr	Pro	Asp	Ser	Arg	Ala	Val	
				260					265					270	
Lys	Pro	Ala	Asp	Arg	Gln	Met	Ala	Gln	Asn	Asn	Ser	Arg	Pro	Glu	
				275					280					285	
Leu	Leu	Asp	Pro	Glu	Pro	Gly	Gly	Leu	Leu	Thr	Ser	Gln	Gly	Phe	
				290					295					300	
Ile	Arg	Leu	Pro	Val	Leu	Gly	Tyr	Ile	Tyr	Arg	Val	Ser	Ser	Val	
				305					310					315	
Ser	Ser	Asp	Glu	Ile	Trp	Leu									
				320											

<210> 73
 <211> 843
 <212> DNA
 <213> Homo Sapien

<400> 73
 cggggacgga agcgggccctt gggcccgagg ggctggagcc gggccggggc 50
 gatgtggagc gcgggccgcg gcggggctgc ctggccggtg ctgttggggc 100
 tgctgctggc gctgttagtg ccggggcggtg gtgccgcaa gaccggtgcg 150
 gagctcgtga cctgcgggtc ggtgctgaag ctgctcaata cgcaccaccg 200
 cgtgcggctg cactcgcacg acatcaaata cggatccggc agcggccagc 250
 aatcggtgac cggcgtagag gcgtcggacg acgccaatag ctactggcgg 300
 atccgcggcg gctcggaggg cgggtgcccg cgcggggtccc cggtgcgctg 350
 cgggcaggcg gtgaggctca cgcattgtgt tacgggcaag aacctgcaca 400
 cgcaccactt cccgtcgccg ctgtccaaca accaggaggt gattgccttt 450
 ggggaagacg gcgagggcga cgacctggac ctatggacag tgcgctgctc 500

tggacagcac tgggagcgtg aggctgctgt gcgcttccag catgtgggca 550
 cctctgtggt cctgtcagtc acgggtgagc agtatggaag ccccatccgt 600
 gggcagcatg aggtccacgg catgcccagt gccaacacgc acaatacgtg 650
 gaaggccatg gaaggcatct tcatcaagcc tagtgtggag ccctctgcag 700
 gtcacgatga actctgagtg tgtggatgga tgggtggatg gagggtaggca 750
 ggtggggcgt ctgcagggcc actcttggca gagactttgg gttttaggg 800
 gtccctcaagt gcctttgtga ttaaagaatg ttggtctatg aaa 843

<210> 74

<211> 221

<212> PRT

<213> Homo Sapien

<400> 74

Met	Trp	Ser	Ala	Gly	Arg	Gly	Gly	Ala	Ala	Trp	Pro	Val	Leu	Leu	1	5	10	15
Gly	Leu	Leu	Leu	Ala	Leu	Leu	Val	Pro	Gly	Gly	Gly	Ala	Ala	Lys	20	25	30	
Thr	Gly	Ala	Glu	Leu	Val	Thr	Cys	Gly	Ser	Val	Leu	Lys	Leu	Leu	35	40	45	
Asn	Thr	His	His	Arg	Val	Arg	Leu	His	Ser	His	Asp	Ile	Lys	Tyr	50	55	60	
Gly	Ser	Gly	Ser	Gly	Gln	Gln	Ser	Val	Thr	Gly	Val	Glu	Ala	Ser	65	70	75	
Asp	Asp	Ala	Asn	Ser	Tyr	Trp	Arg	Ile	Arg	Gly	Gly	Ser	Glu	Gly	80	85	90	
Gly	Cys	Pro	Arg	Gly	Ser	Pro	Val	Arg	Cys	Gly	Gln	Ala	Val	Arg	95	100	105	
Leu	Thr	His	Val	Leu	Thr	Gly	Lys	Asn	Leu	His	Thr	His	His	Phe	110	115	120	
Pro	Ser	Pro	Leu	Ser	Asn	Asn	Gln	Glu	Val	Ser	Ala	Phe	Gly	Glu	125	130	135	
Asp	Gly	Glu	Gly	Asp	Asp	Leu	Asp	Leu	Trp	Thr	Val	Arg	Cys	Ser	140	145	150	
Gly	Gln	His	Trp	Glu	Arg	Glu	Ala	Ala	Val	Arg	Phe	Gln	His	Val	155	160	165	
Gly	Thr	Ser	Val	Phe	Leu	Ser	Val	Thr	Gly	Glu	Gln	Tyr	Gly	Ser	170	175	180	
Pro	Ile	Arg	Gly	Gln	His	Glu	Val	His	Gly	Met	Pro	Ser	Ala	Asn	185	190	195	

Thr	His	Asn	Thr	Trp	Lys	Ala	Met	Glu	Gly	Ile	Phe	Ile	Lys	Pro
				200					205					210
Ser	Val	Glu	Pro	Ser	Ala	Gly	His	Asp	Glu	Leu				
				215					220					

<210> 75
 <211> 1049
 <212> DNA
 <213> Homo Sapien

<400> 75
 gttgctatgt tgcccaggct ggtcttgaag tgccttgacc tcctaaagtg 50
 ttggaaccac agacgtgagc cactccaccc agcctaaaac ttcattcttct 100
 ttggatgaga tgaacacttt taacaagaga acaggactct atataaatcg 150
 ctgtgggctc accacctcta aggaggagca ctgactgaag acagaaaaat 200
 tgatgaactg aagaagacat ggtccattat gccttacaaa cttacacagt 250
 gctttgggaa ttccaaagta ctgagtggag agaggtgttt caggagccgt 300
 agagccagat cgtcatcatg tctgcattgt ggctgctgct gggcctcctt 350
 gccctgatgg acttgtctga aagcagcaac tggggatgct atggaaacat 400
 ccaaagcctg gacacccctg gagcatcttg tgggattgga agacgtcacg 450
 gcctgaacta ctgtggagtt cgtgcttctg aaaggctggc tgaaatagac 500
 atgccatacc tcctgaaata tcaacccatg atgcaaacca ttggccaaaa 550
 gtactgcatg gatcctgccg tgatcgctgg tgtcttgtcc aggaagtctc 600
 ccggtgacaa aattctggct aacatgggag ataggactag catggtgcag 650
 gaccctggct ctcaagctcc cacatcctgg attagtgagt ctcaggtttc 700
 ccagacaact gaagttctga ctactagaat caaagaaatc cagaggaggt 750
 ttccaacctg gaccctgac cagtacctga gaggtggact ctgtgcctac 800
 agtgggggtg ctggctatgt ccgaagcagc caggacctga gctgtgactt 850
 ctgcaatgat gtccttgac gagccaagta cctcaagaga catggcttct 900
 aacatctcag atgaaacca agaccatgat cacatatgca gcctcaaatg 950
 ttacacagat aaaactagcc aagggcacct gtaactggga atctgagttt 1000
 gacctaaaag tcattaaaat aacatgaatc ccattaaaaa aaaaaaaaaa 1049

<210> 76
 <211> 194
 <212> PRT
 <213> Homo Sapien

<400> 76

Met	Ser	Ala	Leu	Trp	Leu	Leu	Leu	Gly	Leu	Leu	Ala	Leu	Met	Asp
1				5					10					15
Leu	Ser	Glu	Ser	Ser	Asn	Trp	Gly	Cys	Tyr	Gly	Asn	Ile	Gln	Ser
				20					25					30
Leu	Asp	Thr	Pro	Gly	Ala	Ser	Cys	Gly	Ile	Gly	Arg	Arg	His	Gly
				35					40					45
Leu	Asn	Tyr	Cys	Gly	Val	Arg	Ala	Ser	Glu	Arg	Leu	Ala	Glu	Ile
				50					55					60
Asp	Met	Pro	Tyr	Leu	Leu	Lys	Tyr	Gln	Pro	Met	Met	Gln	Thr	Ile
				65					70					75
Gly	Gln	Lys	Tyr	Cys	Met	Asp	Pro	Ala	Val	Ile	Ala	Gly	Val	Leu
				80					85					90
Ser	Arg	Lys	Ser	Pro	Gly	Asp	Lys	Ile	Leu	Val	Asn	Met	Gly	Asp
				95					100					105
Arg	Thr	Ser	Met	Val	Gln	Asp	Pro	Gly	Ser	Gln	Ala	Pro	Thr	Ser
				110					115					120
Trp	Ile	Ser	Glu	Ser	Gln	Val	Ser	Gln	Thr	Thr	Glu	Val	Leu	Thr
				125					130					135
Thr	Arg	Ile	Lys	Glu	Ile	Gln	Arg	Arg	Phe	Pro	Thr	Trp	Thr	Pro
				140					145					150
Asp	Gln	Tyr	Leu	Arg	Gly	Gly	Leu	Cys	Ala	Tyr	Ser	Gly	Gly	Ala
				155					160					165
Gly	Tyr	Val	Arg	Ser	Ser	Gln	Asp	Leu	Ser	Cys	Asp	Phe	Cys	Asn
				170					175					180
Asp	Val	Leu	Ala	Arg	Ala	Lys	Tyr	Leu	Lys	Arg	His	Gly	Phe	
				185					190					

<210> 77

<211> 899

<212> DNA

<213> Homo Sapien

<400> 77

ttgaaaatct actctatcag ctgctgtggt tgccaccatt ctcaggaccc 50

tcgccatgaa agcccttatg ctgctcacc tgtctgttct gctctgctgg 100

gtctcagctg acattcgctg tcaactcctgc tacaaggtcc ctgtgctggg 150

ctgtgtggac oggcagtcct gccgcctgga gccaggacag caatgcctga 200

caacacatgc ataccttggt aagatgtggg ttttctccaa tctgcgctgt 250

ggcacaccag aagagccctg tcaggaggcc ttcaaccaa ccaaccgcaa 300

gctgggtctg acatataaca ccacctgctg caacaaggac aactgcaaca 350
gcgcaggacc ccggcccact ccagccctgg gccttgtctt ccttacctcc 400
ttggtctggc ttggcctctg gctgctgcac tgagactcat tccattggt 450
gccccctctc ccacctgcct tggcctgagc ctctctccct gtgtctctgt 500
atccccctggc ttacagaat cgtctctccc tagctcccat ttctttaatt 550
aaacactgtt ccgagtggtc tcctcatcca tccttcccac ctcacacct 600
tcactctcct ttttctgggt cccttcccac ttccttccag gacctccatt 650
ggctcctaga agggctcccc actttgcttc ctatactctg ctgtccccta 700
cttgaggagg gattgggatc tgggcctgaa atggggcttc tgtgttgtcc 750
ccagtgaagg ctcccacaag gacctgatga cctcactgta cagagctgac 800
tccccaaacc caggctccca tatgtacccc atcccccata ctcacctctt 850
tccattttga gtaataaatg tctgagtctg gaaaaaaaaa aaaaaaaaaa 899

<210> 78
<211> 125
<212> PRT
<213> Homo Sapien

<400> 78
Met Lys Ala Leu Met Leu Leu Thr Leu Ser Val Leu Leu Cys Trp
1 5 10 15
Val Ser Ala Asp Ile Arg Cys His Ser Cys Tyr Lys Val Pro Val
20 25 30
Leu Gly Cys Val Asp Arg Gln Ser Cys Arg Leu Glu Pro Gly Gln
35 40 45
Gln Cys Leu Thr Thr His Ala Tyr Leu Gly Lys Met Trp Val Phe
50 55 60
Ser Asn Leu Arg Cys Gly Thr Pro Glu Glu Pro Cys Gln Glu Ala
65 70 75
Phe Asn Gln Thr Asn Arg Lys Leu Gly Leu Thr Tyr Asn Thr Thr
80 85 90
Cys Cys Asn Lys Asp Asn Cys Asn Ser Ala Gly Pro Arg Pro Thr
95 100 105
Pro Ala Leu Gly Leu Val Phe Leu Thr Ser Leu Ala Gly Leu Gly
110 115 120
Leu Trp Leu Leu His
125

<210> 79

<211> 1977
<212> DNA
<213> Homo Sapien

<400> 79

acgggcccga gcggcagtg cgtaggggtg gcgcacggat ccgttgcggc 50
tgcagctctg cagtcggggc gttccttcgc cgccgccagg ggtagcggtg 100
tagctgcgca gcgtcgcgcg cgctaccgca cccaggttcg gcccgtaggc 150
gtctggcagc ccgggcgcat cttcatcgag cgccatggcc gcagcctgcg 200
ggccggggagc ggccgggtac tgcttgctcc tcggcttgca tttgtttctg 250
ctgaccgcgg gccctgccct gggctggaac gaccctgaca gaatgttgct 300
gcgggatgta aaagctctta ccctccacta tgaccgctat accacctccc 350
gcaggctgga tcccatccca cagttgaaat gtgttgaggg cacagctggg 400
tgtgattctt ataccccaaa agtcatacag tgtcagaaca aaggctggga 450
tgggtatgat gtacagtggg aatgtaagac ggacttagat attgcataca 500
aatttgaaa aactgtggtg agctgtgaag gctatgagtc ctctgaagac 550
cagtatgtac taagaggttc ttgtggcttg gagtataatt tagattatac 600
agaacttggc ctgcagaaac tgaaggagtc tggaaagcag cacggctttg 650
cctctttctc tgattattat tataagtggc cctcggcgga ttcctgtaac 700
atgagtggat tgattaccat cgtgggtact cttgggatcg cctttgtagt 750
ctataagctg ttcttgagtg acgggcagta ttctcctcca ccgtactctg 800
agtatcctcc attttcccac cgttaccaga gattcaccaa ctcagcagga 850
cctcctcccc caggctttaa gtctgagttc acaggaccac agaatactgg 900
ccatggtgca acttctgggt ttggcagtg ttttacagga caacaaggat 950
atgaaaattc aggaccaggg ttctggacag gcttggaac tgggtggaata 1000
ctaggatatt tgtttggcag caatagagcg gcaacaccct tctcagactc 1050
gtggtactac ccgtcctatc ctccctccta ccctggcacg tggaaatagg 1100
cttactcacc cttcatgga ggctcgggca gctattcggg atgttcaaac 1150
tcagacacga aaaccagaac tgcacagga tatggtggta ccaggagacg 1200
ataaagtaga aagttggagt caaacactgg atgcagaaat tttggatttt 1250
tcactacttt ctctttagaa aaaaagtact acctgttaac aattgggaaa 1300
aggggatatt caaaagttct gtggtgttat gtccagtgtg gctttttgta 1350

ttctattatt tgaggctaaa agttgatgtg tgacaaaata cttatgtggt 1400
 gtatgtcagt gtaacatgca gatgtatatt gcagtttttg aaagtgatca 1450
 ttactgtgga atgctaaaaa tacattaatt tctaaaacct gtgatgccct 1500
 aagaagcatt aagaatgaag gtgttggtact aatagaaact aagtacagaa 1550
 aatttcagtt ttaggtgggt gtagctgatg agttattacc tcatagagac 1600
 tataatattc tatttggtat tatattattt gatgtttgct gttcttcaaa 1650
 catttaaate aagctttgga ctaattatgc taatttgatga gttctgatca 1700
 cttttgagct ctgaagcttt gaatcattca gtggtggaga tggccttctg 1750
 gtaactgaat attaccttct gtaggaaaag gtggaaaata agcatctaga 1800
 aggttggtgt gaatgactct gtgctggcaa aaatgcttga aacctctata 1850
 tttctttcgt tcataagagg taaagggtcaa atttttcaac aaaagtcttt 1900
 taataacaaa agcatgcagt tctctgtgaa atctcaaata ttgttgtaat 1950
 agtctgtttc aatcttaaaa agaataca 1977

<210> 80
 <211> 339
 <212> PRT
 <213> Homo Sapien

<400> 80
 Met Ala Ala Ala Cys Gly Pro Gly Ala Ala Gly Tyr Cys Leu Leu
 1 5 10 15
 Leu Gly Leu His Leu Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly
 20 25 30
 Trp Asn Asp Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu
 35 40 45
 Thr Leu His Tyr Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro
 50 55 60
 Ile Pro Gln Leu Lys Cys Val Gly Gly Thr Ala Gly Cys Asp Ser
 65 70 75
 Tyr Thr Pro Lys Val Ile Gln Cys Gln Asn Lys Gly Trp Asp Gly
 80 85 90
 Tyr Asp Val Gln Trp Glu Cys Lys Thr Asp Leu Asp Ile Ala Tyr
 95 100 105
 Lys Phe Gly Lys Thr Val Val Ser Cys Glu Gly Tyr Glu Ser Ser
 110 115 120
 Glu Asp Gln Tyr Val Leu Arg Gly Ser Cys Gly Leu Glu Tyr Asn
 125 130 135

Leu	Asp	Tyr	Thr	Glu	Leu	Gly	Leu	Gln	Lys	Leu	Lys	Glu	Ser	Gly	
				140					145					150	
Lys	Gln	His	Gly	Phe	Ala	Ser	Phe	Ser	Asp	Tyr	Tyr	Tyr	Lys	Trp	
				155					160					165	
Ser	Ser	Ala	Asp	Ser	Cys	Asn	Met	Ser	Gly	Leu	Ile	Thr	Ile	Val	
				170					175					180	
Val	Leu	Leu	Gly	Ile	Ala	Phe	Val	Val	Tyr	Lys	Leu	Phe	Leu	Ser	
				185					190					195	
Asp	Gly	Gln	Tyr	Ser	Pro	Pro	Pro	Tyr	Ser	Glu	Tyr	Pro	Pro	Phe	
				200					205					210	
Ser	His	Arg	Tyr	Gln	Arg	Phe	Thr	Asn	Ser	Ala	Gly	Pro	Pro	Pro	
				215					220					225	
Pro	Gly	Phe	Lys	Ser	Glu	Phe	Thr	Gly	Pro	Gln	Asn	Thr	Gly	His	
				230					235					240	
Gly	Ala	Thr	Ser	Gly	Phe	Gly	Ser	Ala	Phe	Thr	Gly	Gln	Gln	Gly	
				245					250					255	
Tyr	Glu	Asn	Ser	Gly	Pro	Gly	Phe	Trp	Thr	Gly	Leu	Gly	Thr	Gly	
				260					265					270	
Gly	Ile	Leu	Gly	Tyr	Leu	Phe	Gly	Ser	Asn	Arg	Ala	Ala	Thr	Pro	
				275					280					285	
Phe	Ser	Asp	Ser	Trp	Tyr	Tyr	Pro	Ser	Tyr	Pro	Pro	Ser	Tyr	Pro	
				290					295					300	
Gly	Thr	Trp	Asn	Arg	Ala	Tyr	Ser	Pro	Leu	His	Gly	Gly	Ser	Gly	
				305					310					315	
Ser	Tyr	Ser	Val	Cys	Ser	Asn	Ser	Asp	Thr	Lys	Thr	Arg	Thr	Ala	
				320					325					330	
Ser	Gly	Tyr	Gly	Gly	Thr	Arg	Arg	Arg							
				335											